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             PLARIGVASKLLS"
BASE COUNT   399 a      414 c      379 g      371 t
ORIGIN
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Matches 1257;   Conservative   0;   Mismatches   302;   Indels   9;   Gaps   2;

Query Match   55.2%;   Score 1046.8;   DB 8;   Length 1563;
Best Local Similarity 80.2%;   Pred. No. 1.8e-290;

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Qy   144 ATGTTGGTGAACTTGCAATTACTCTGGTTGGTGATAGCCGTTGTTCATCACACCTGCGTCCC 203
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Db     1 ATGTTGCTGGAACTTGCACTTGGTTGTTGTTGTTGTTAGCTTTGTTTCTCCACTTGCGTCCC 60

Qy   204 ACACTAAGTGCAAAATCAAAGCACTTCCCTTGCCACCTCCCAAACCCTCCAAGTCCAAAACCC 263
         |||| ||| |||||||||||||||||||| | ||||||||||||||| ||||| ||
Db    61 ACACCAAGCGCAAAATCAAAAGCACTTCCGGTTGCCACCTCCCAAACCCTCCAAGCCCAAAGCCT 120

Qy   264 CGTCTCCCATTGTGGGTCACCTTCACCTTTAGACAAAGCCCTTCTCCACTACTCCCTC 323
         ||||| |||| || || || |||| ||||||||||||||||| | ||||||||||||
Db   121 CGTCTTCCCTTCATTGGCCACCTTCACCTTCTTTAAAAGATAAACTTCTCCACTATGCACTC 180

Qy   324 ATCGACCTAAGCACAAACGCTATGGTCCCGTTACTCCCTCTACTTCGGTTCCATGCCAACC 383
         ||||||| |    || ||  ||| |||||||||||||||||| | |||||||||||||
Db   181 ATCGATCTCTCCAAAAAGCATGGCCCCCTATTCTCTCTCTCCTTTCGGCTCCATGCCCAACC 240

Qy   384 GTTGTAGCCTTCACCCCTGAACTTTCAAAACTCTTCCTCCAAACTCACGAGGCCTCTTCC 443
         |||| | || ||||||| ||||| ||| | |||||| |||||||||||||||||  || |
Db   241 GTCGTTGCCCTCACCCCTGAGTGTTCAAGCCTCTTCCTGGGAGGAGCAACTTCC 300

Qy   444 TTCAACAAGGTTCCAAACCTCTGCCATTAGGCGCCTAACCTACGGACAACTCTGTTGCC 503
         || |||||| |||||||||| |||||| || || || ||| || |||||||||||||||
Db   301 TTCAGCAAGAGTTCCAAACCTCGCGTAAGACGCCTCACTTACGGACAACTCTGTGGCC 360

Qy   504 ATGGTTCCCTTGGTCCTTACTGGAAGTTCATTAGGAAGCTCATCATGAACGACGACCTCCTC 563
         |||||||  | |||||| ||||| |||| |   ||| |||||||||||||||||||  |||
Db   361 ATGGTTCCATTCGGAGCCTTACTGGAAGTTCGTGAGAAGCTCATCATGAACGACCTTCTC 420

Qy   564 AATGCCACAACTGTGAACAAGTGAACGTTGAGCCCTTTAAGGAGCCAAGAAATCCGAAAGTCCTC 623
         || ||||||||  | || |||| |   |||| ||||| |||||||||||||||||||||||
Db   421 AACGCCACAACCGTCAACGAGCTCAGACCGCTCAGGACCCAACAGATCCGCCAAGTTCCTT 480

Qy   624 AGGGTGATGGCACAGAGTGCTGAGTCTGAGTTCCAGTCCCAACTTAATGTCACGGAGAGCTTCTC 683
         || ||||||||||| |  |||| |  ||| ||||||||| | | |||| ||| ||||||||||
Db   481 AGGGTTATGGCCCAAGAGCGCAGAGGCCCAGAAGCCCCTTGACGTCACAGAGGAGCTTCTC 540

Qy   684 AAGTGGACCAACAGCACCATCTCGAGGATGATGATGGGTGGGAAGCCAGAGGAAATCAGGGAC 743
         ||| ||||||||||||| ||||| |||||| | ||||| ||  ||| ||| |||||||| ||
Db   541 AAATGGACCAACAGCACCATCTCCATGATGATGATGGGAGGAGCTGAGGAGATCAGAGAC 600

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Db   601 ATCGCTCGCGAGGTCCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT 660

Qy   804 TTGAAGAAACTCAAGGTTGGGCAATACGAGAAGAGGATTGACGATATTATTCAACAGTTT 863
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Db   661 TTGAAGTATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTTGAACAAGTTC 720

Qy   864 GACCCCGTCATTGAGAGGGTCATCAAGAAAAGAAGACAGGAGATTAGGAGGAGGAAGAAG 923
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Db   721 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTCAGGAGGAGAAA---- 776
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Qy   924 AGGAATGGTGAGATCGAGGAGGTGAACAGAGTGTGTTTTCTCGACACTTTGCTCGAT 983
         ||  ||| || ||| || |||| || || || | ||   ||||||||||||| ||
Db   777 --GAACCGAGAAGTGTTGAGGGCGAGGCCAGCGGCGTCCTCCGACACTTTGCTTGAA 834
         || |  || | |   | || ||||  | || || ||||||||||||||  ||||||
Qy   984 TTTGCTGAGGACGAGACCATGGAGATCAAAATCACCAAGGACAAATCAAGGGCCTTGTT 1043
         || ||  |||||||||||||| |||||| | ||||||||| |||| |||| ||||||||
Db   835 TTCGTGAGGACGAGACCATGGAGATCAAAATTACCAAGGAGCAAATCAAGGGCCTTGTT 894
         || ||  |||||||||||||||||||||||  |||||||||||||||||||||||||||
Qy  1044 GTGGATTTCTTCTCAGCAGGTAGTGACTCCACCGCGTGGCAACAGACTGGGCTCTGTCA 1103
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Db   895 GTCGACTTTTTCTCTGCAGGACAGATTCCACCAGCGGTGGCAACAGAGTGGGCATTGGCA 954
         || || |||||||| ||||| || ||||| |||| || ||||||||| |  ||||| ||
Qy  1104 GAGCTCATCAACAACACCCAGGTGTTCAAAAGGCACGAGGAGATCGTGAGGAACCTTCCTT 1163
         |||||||| ||| || ||  ||||| |||||| ||||| ||  || ||||| |||||  |
Db   955 GAGCTCATCAACAACACCCAGGGTGTTCAAAAGGCTCGTGAGGAGGTTCACAGTGTTGTG 1014
         |||||||||||||||||||||| ||||||||||| || || |||| ||| |||||||||
Qy  1164 GGAAAAGACAGACTCGTTGACGAGGCAGATGTCGAGAACCTTCCTTACATTGAGATCCATC 1223
         ||||| ||| ||  |  || ||||||||| || | ||  |  | |||| | || |||||
Db  1015 GGCAAAGATAGACTCGTTGACGAGTCGACTCGCACACTCAAAACCTTCCTTACATTGCGCATT 1074
         || |||||| |||||||||||||| | || |  | |  ||| |||| | |||| |  |||
Qy  1224 GTGAAGGAGACGTTCCGCATGCACCCACCACCCTTCCCGTGGTCAAAAGAAAGTGCGTGCAG 1283
         ||||||||||| | || |||||  | || || ||||||||||||||| |||| ||| |||
Db  1075 GTGAAGGAGACATTCCGAATGCACCCACCACCCCTTCCCGTGGTCAAAAGAAAGTGCGTGCAG 1134
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Qy  1284 GAGTGTGAGTGCGACGGTTATGTGATCCCAGAGGGAGCAGCATTGATCCTTTCAATGTTGG 1343
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Db  1135 GAGTGTGAGATTAATGGGTATGTGATCCCAGAGGGAGCAGCATTGTTCTTTCAATGTTTGG 1194
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Qy  1344 GCCGTGCGGAGAGAGACCCAAATACTGGGACAGGCCCACTGAGTTCCCGTCCCGAAAGGTTC 1403
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Db  1195 CAAGTAGGAAAGGACCCAAATACTGGGACAGGCCAATCAGAATTCCGTCCCGAGAGGTTC 1254
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Qy  1404 TTAGAAAATGTGGGTGAAGGGGATCAAG--CCGTGACCTTAGGGTGTCAACATTCCAAC 1460
         ||||| | | ||| ||||| ||||   || | ||  ||||| ||  ||| ||||||||
Db  1255 TTAGAAACTGGCGCGTGAAGGGAGCCAGGGGCCCTCTTGATCTTTAGGGCCAGCATTTCCAA 1314
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Qy  1461 CTTCTTCCGTTGGGTGCTGGAAGGAGGATGTGCCCTGGCGTCAATTTGGCCACTGCGCGGGA 1520
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Db  1315 CTCTCCCATTTGGGTCTCGGGGAGGAGAATGTGCCCTGGTGTCAATTTGGCTACTTCAGGA 1374
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Qy  1521 ATGGCCACACTGCTTGCGTCAGTTATCCAGTGCTTTGATCTCCAGTGGTGGGCCCACAG 1580
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Qy  1581 GGAAAGATATTGAAGGGCAATGACGCTCAAGGTCACGGGACTCACG 1640
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Db  1435 GGACAAATATTGAAAGTGACGATGCCAAAGTTAGCATGGAAGAGAGCTGGCCTCACC 1494
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Qy  1641 GTTCCAAGGGCACATAACCTCATCTGTGTCCCGGTTGCAAGATCAAGTGCCGTACCCAAA 1700
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Db  1495 GTTCCAAGGGCCACATAGTCTGTGTTGTGTTCCCACTGTGCAAGGATCGCGGTTGTCATCTAAA 1554
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Qy  1701 CTCTTTTC 1708
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Db  1555 CTCCTTTC 1562
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RESULT 7
AF135484
LOCUS       AF135484                 1722 bp    mRNA    linear    PLN 02-AUG-1999
DEFINITION  Glycine max cytochrome P450 monooxygenase CYP93C1v2p (CYP93C1v2)
            mRNA, complete cds.
ACCESSION   AF135484
VERSION     AF135484.1   GI:5059123
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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REFERENCE   Glycine.
             1 (bases 1 to 1722)
AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
TITLE   Molecular characterization of the enzyme catalyzing the aryl
             migration reaction of isoflavonoid biosynthesis in soybean
JOURNAL   Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
MEDLINE   99306846
PUBMED   10375412
REFERENCE   2 (bases 1 to 1722)
AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
TITLE   Direct Submission
JOURNAL   Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam
             Noble Pkwy, Ardmore, OK 73402, USA
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                     AF022462; causes change of E to K (aa 295)"
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BASE COUNT   470 a   422 c   407 g   423 t
ORIGIN

Query Match   55.0%; Score 1041.6; DB 8; Length 1722;
Best Local Similarity 79.6%; Pred. No. 5.7e-289;
Matches 1259; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

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Qy   138 AACACCATGTTGCAACTGGTGGAACTTGCAATTACTCTGTTGGTATAGCCCTGTTCATACACCTG 197
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Db    30 AACACGATGTTGCTTGAACTTGCACTTGCACTTCCCATTGGTTTTTGGCTCGTTTTCTGCACTTG  89

Qy   198 CGTCCCACACTAAGTGCAAAATCAAAGTCCCTTCGCCACCTCCAAACCCTCCAAGTCCA 257
             ||||||||| ||||||||| | |||||||||||| ||||||||||||||||| ||
Db    90 CGTCCCACACCCACGTGCAAAATCAAAAGCACTTCCGCCCATCTCCAAACCCACCAAGCCCCA 149
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Qy 258 AAACCCCGTCTCCATTGTGGGTCACCTTCACCTTTTTGAGACAAACCCCTTCTCCACTAC 317
            |||| || ||||||| || || ||||||| ||||| || | ||| |||||||||||||
Db 150 AAGCCTGTCTCCCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTAC 209

Qy 318 TCCCTCATCGACCTAAGCAACGCTATGGTCCGCGTTTACTCCCTCACTTTTGGTTCCATG 377
            |||||||||||| ||| ||||||||| ||| |||||||||||||||| |||||||
Db 210 GCACTCATCGACCTCCAAAAAACATGGTCCCTTTATTCTCTCTCTACTTTGGCTCCATG 269

Qy 378 CCAACCGGTTGTAGCCTCCACCCTGACTTTCAAACTCTTCCTCCAAACTCACGAGGCC 437
            |||||||| ||||||||||||||| |||| ||||||||||| ||||||||| |||||||
Db 270 CCAACCGGTTGTGCCTCCACCACCAGAATTGTTCAAGCTCTTCCTCCAAACCACGAGGCA 329

Qy 438 TCTTCCTTCAACACAAGTTCCAAACCTCTGCCATTAGGCGCCTAACCTACGACAACTCT 497
            |||||||||||||||||||||||||||||| ||||| ||||| |||||||| || |||
Db 330 ACTTCCTTCAACACAAGGTTCCAAACCTCAGCCATATAAGACGCCTCACCTATGATAGCTCA 389

Qy 498 GTTGCCATGGTTCCCTTGGTCCTTACTGAAGTTCATTAGGAAGTCATCATGACGAC 557
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Db 390 GTGGCCATGGTTCCCTTCGCGACCTTACTGGAGTTCGTGAGGAAGCTCATCATGAACGAC 449

Qy 558 CTCCTCAATGCCACACAGTGTCGAGGCCTTTAAGGAGCCAAGAAATCCGAAAG 617
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Db 450 CTTCTCAACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAG 509

Qy 618 GTCCTCAGGGTGATGGCACAGAGTGCTGAGTCTCAGGTCCCACTTAATGTCACCGAGGAG 677
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Db 510 TTCCTTAGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAG 569

Qy 678 CTTTCAAGTGACCAACAGCACCATCTCGAGGATGATGCTTGGGGAGCAGAGGAAATC 737
            |||| | || || |||||| |||||| |||| ||||| |||||||||||||||| ||
Db 570 CTTCTGAAATGACCAACAGCACCATCCCATGATGATGATGTCTCGCGGAGCGTGAGGAGATC 629

Qy 738 AGGGACATAGCACGTGACGTGCTTGTTAAGATCTTTGGGGAGTATAGTCTCACCGACTTCTC 797
            || |||| || | ||| || || | | ||||||| || |||||||||||||||| |||||
Db 630 AGAGACATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATCAGCCTCACTGACTTCATC 689

Qy 798 TGGCCCTTGAAGAAACTCAAGGTTGGCAATACGAAGAGAGATTGACGATATATTCAAC 857
            ||||||||||||| |||||||||||||| |||| |||||| ||| || || ||||||||
Db 690 TGGCCATTGAAGCATCTCAAGGTGAAAGTATGAAAGTATGAAAGATGCGACGACATCTTGAAC 749

Qy 858 AGGTTGTGACCCCGTCATTGAGAGGGTCATCAAGAAAAGACAGAGGATTAGGAAGAAGAGG 917
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Db 750 AAGTTCGACCCTGTCGTTGAAGGGTCATCAAGAAGAGAGAGAAGAAGCGCCGTGAGGAGAGA 809

Qy 918 AAGGAGAGAATGGTGAGATCGAGAGGGATCGAGAGGACCATGGAGATCAAAATCAAGGGC 977
            |||| || ||||||| |||||||| ||||||||| | ||| |||| ||| ||||||| ||
Db 810 AA------GAACGGAGAGGTTGTTGGAGGGGAGGTCAGCGGGGTTTTCCTTGACACTTTG 863

Qy 978 CTCGATTTTGCTGAGGACGAGACCATGGAGATCAAAATCAAAGGAACAGCCACCATCAAGGGT 1037
            || ||| || |||||||||||| ||||||||| |||||| ||||||| |||| |||||||||
Db 864 CTTGAATTCGCTGAGGATGAGACATGGAGATCAAAATCAAAACACCAAGGACCACATCAAGGGT 923

Qy 1038 CTTGTTGTGGATTTCTTCTCAGCAGGAACCACCGGTGTTGCTAAGGGAACAGACTGGCT 1097
             |||||||| |||||||| |||||||||||| ||||||| |||| ||||| ||||||
Db 924 CTTGTTGTCGACTTTTTCTCCGCAGGAACCGACAGCACTGCAGTCGCAACGAGAGCTGGCCA 983

Qy 1098 CTGTCAGGAGCTCATCAACAACACCCAGGTGTTCAACAACATCCTAAGGTGTTGGAAAGGAG 1157
             ||||| ||||| |||| ||||| || |||||| ||||| |||| ||||| ||||||||
Db 984 TTGGCAGAACTCATCAACAACATCCTAAGGTGTTGGAAAGGTCGTGAGGAGGTCTCAGT 1043

Qy 1158 GTCGTGGGAAAAGACAGACTCCGTTGACGAGGCAGATGTCCAGAACCTTCCTTACATTAGA 1217
             | |||||||||| ||| ||||| | | | | ||||||| |||||| || |||||||| |
Db 1044 GTTGTGGGAAAGGACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGA 1103

Qy 1218 TCCATCGTGAAGGAGACGTTCCGCATGCACCCGTTCATCATACACCTG 1277
             ||||| |||||||||| || || |||| | || ||||||| |||||||
Db 1104 GCAATCGTGAAGGAGACATTCCGCATGCACCCGTTTGGCTCAAAGAAGTGC 1163

Qy 1278 GTGCAGGAGTCTGAGGTCGACGGTTATGTGATCCGAGGAGGAGCATTGATCCTTTTCAAT 1337
             |||||||| ||||||| | | |||||| ||||| |||||| | |||| ||| |||||
Db 1164 ACAGAAGAGTGTGAGATTAATGGTATATGTGATTCCCGAGGAGGAGCATTGATTCTCTTCAAT 1223

Qy 1338 GTTTGGGCCGTCGGAAGAGACCCAAAATACTGGAAGAGATCCACTGAGTTCCGTCCCGAA 1397

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BASE COUNT   497 a   448 c   416 g   463 t
ORIGIN

Query Match   54.7%;   Score 1036.8; DB 8;   Length 1824;
Best Local Similarity 79.4%; Pred. No. 1.4e-287;
Matches 1256; Conservative 0; Mismatches 317; Indels 9; Gaps 2:

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Qy   138 AACACCATGTGGTGGAACTTGCAATTACTCTGTTGGTGATAGCCGTGTTCATACACCTG  197
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Db    48 AACACGATGTTGCTTGACACTTCTGAACTTGCTTTATTGGTTTGGCTCTGTTCTGCACTTG  107

Qy   198 CGTCCCACACTAAGTGCAAAATCAAAGTCCCTTGCGCCACCTCCAAACCTCCAAGTCCA  257
         |||| ||||| |||||||||||   |||||||| || ||| || || |||||||||||
Db   108 CGTCCCACACCACTGACAAAATCAAAAGCACTTCCCATCTCCCAAACCCACCAAGCCCA  167

Qy   258 AAACCCGTCTCCATTGTGGTGCACCTCACCTTTAGACAAACCCCTTCTCCACTAC  317
         || ||| ||||||| || ||  || ||  ||||| ||||||||  ||||||||||
Db   168 AAGCCTCGTCTCCCTTCATCTTCATAGGACACCTCATCTCTAAAAGACAAACTTCTCCACTAC  227

Qy   318 TCCCTCATCGACCTAAGCAAAGCTATGTCCGCTTACTCCCTTACTCGGTTCCATG  377
         ||||||||||||| ||||||| ||||||| ||||||| || |||| |||||||||
Db   228 GCACTCATCGACCTCTCCAAAAAACATGGTCCCTTATCTCTCCTTACTTGGCGTCCATG  287

Qy   378 CCAACCGTTGTGAGCCTCCACCCCTGAACTTTCAAACTCTTCCTCCAAACTCACGAGGCC  437
         |||||||||||| |||||||   |||| ||| |||| |||||||||  |||| ||||||
Db   288 CCAACCGTTGTGCCTCCAACAGAATTGTTCAAGCTCTTCCTCCCAAACGCACGAGGCA  347

Qy   438 TCTTCCTTCAACAAGGTCCAAACCTCTGCCAACCTTAGGCGCTAACCTACGACGACAACTCT  497
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Db   348 ACTTCCTTCAACAACAGGTTCCAAACCTCACCTATGATAGCTCA  407

Qy   498 GTTGCCATGGTTCCCTTGGTCCTTACTGGAAGTCATTAGGAAGCTCATCATGAACGAC  557
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Db   408 GTGTGAGCCATGGTTCCCTTCGCGACCTTACTGGAAGTTCGTGGAAGCTCATCATGAACGAC  467

Qy   558 CTCCTCAATGCCACAACTGTGAACAAGTTGAGGCCTTAAGGAGCCAAGAAATCCGAAAG  617
         || || || |||||||||| ||||||||||||||| | ||||| ||    |||| |||
Db   468 CTTCCCAACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGCCTTTGAGGACCCCAAGCAAG  527

Qy   618 GTCCTCAGGTGGATGGCACAGAGTGCTGAGTCTCAGGTCCCACTTAATGTCACCGAGGAG  677
         | || |||| | |||||   || ||||||   |||| ||| || |||| ||||||||||
Db   528 TTCCTTAGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCTTGACTGACCGAGGAG  587

Qy   678 CTTCTCAAGTGACCAACAGCACCATCTCGAGATGATGCTTGGGGAGCAGAGCAGAAATC  737
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Db   588 CTTCTGAAATGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATC  647

Qy   738 AGGGACATAGCACGTGACGTGCTTAAGATCTTTGGGAGTATAGTTCTCACCGACTTCATC  797
         ||||| || || ||||| ||| ||||||||||||  ||||| ||| ||| |||||||||
Db   648 AGAGACATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATC  707

Qy   798 TGGCCCTTGAAGAAACTCAAGGTTGGGCAATACGAAGAAGAGGATTGACGATATTCAAC  857
         ||||| |||||| | |||||||||| ||  ||||| ||||||||| |||| ||| |||
Db   708 TGGCCATTGAAGCATCTCAAGGTTGGAAAGTATGAAAAGAGGATCGACGACATCTTGAAC  767

Qy   858 AGGTTTGACCCCGTCATTGAGAGGGTCATCAAGAAAAGACAGGAGATTAGGAGAAGAGG  917
         | |||||||||  ||| ||| ||||||||||||| |  | | |||| | ||||| |||
Db   768 AAGTTCGACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGA  827

Qy   918 AAGGAGAGGAATGTGAGATCGAGGAGGTGAACAGAGTTGTGGTTTTTCTCGACACTTTG  977
         ||  |  || || || || | |||||||| | |  ||||||  ||| || ||||||||
Db   828 AA------GAACGGAGAGGTTGTTGAGGGTGAGGTGAGTGGGTTTTCCTTGACACTTTG  881

Qy   978 CTCGCATTTGCTGCTGCTGGTGATTTCTTCTCAGCAGGACGAGGATCAAAATCAAGGGC  1037
         || ||| || |||| |||| ||| || ||||||||||||||| ||||||| || || |
Db   882 CTTGAATTCGCTGAGGATGAGATCAGAGATCAAAATCACCAAGGACCAAAATACCAGAGGGT  941

Qy  1038 CTTGTTGTGTGATTTCTTCTCAGCAGGACGGACCGATTCCACGGCGGTGCAACAGACTGGGCT  1097
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Db  1224 GTATGGCAAGTAGGAGAGACCCCAAATACTGGGACACAGCCATCGGAGTTCCGTCCTGAG  1283
         || ||| |||| || || |||| |  ||||||| || |  || || || |||||||||||
Qy  1398 AGGTCTTAGAAAATGTGGCGAAGGGATCAAG---CCGTTGACCTTAGGGTGCAACAT  1454
         |||| || ||  ||||| ||||||||||| ||    ||| |||||||||| |||||||
Db  1284 AGGTTCCTAGAGACAGGGCTGAAGGGGAACAGGGCCCTCCTTGATCTTAGGGACAACAT  1343

Qy  1455 TTCCAACTTCTTCCGTTTGGGTCTGGAAGGAGGATGTGCCCTGGCGTCAATTGGCCACT  1514
         || ||||||||| || |||||||||| ||||| ||||||||||| |||||| ||| ||
Db  1344 TTTCAACTTCTCCCCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACT  1403

Qy  1515 GCGGGAATGGCCACACTGCTGCCTCAGTGCTCTATCCAGTGCGTTGATCTCAGCGAGTGGGC  1574
         | |||||||||  |||| || | ||||| |||||  |||||| | ||| | || |||||||
Db  1404 TCGGGAATGGCAACACTTCTTCGTGCATCTTATTCAGTGCTTCGACTTGCAAGTGCTGGGT  1463

Qy  1575 CCACAGGGAAAGAGATATTGAAGGGCAATGATGCCAAGGTTAGCATGGAAGAGAGCTGA  1634
         ||||||| | |||||||||||||||  ||||||||||| ||||||||||||||||| |
Db  1464 CCACAGGACGAGATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGCCGGC  1523

Qy  1635 CTCACGGTTCCAAGGGCACATAACCTCATCTGTCCCGTTGCAAGATCAAGTGCCGTA  1694
         |||| |||||||||||||||||  |||| | || |  || ||||||| |||| ||
Db  1524 CTCACTGTTCCAAGGGCACATAGTCTCTTGTCTGTGTTCCACTTGCAAGATCGGCGTTGCA  1583

Qy  1695 CCCAAACTCTTTTCGTCGTAAA  1716
         |||||||||  ||  |  |||
Db  1584 TCTAAACTCCTTTCTTAATTAA  1605
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RESULT 8
AF022462
LOCUS   AF022462   1824 bp   mRNA   linear   PLN 02-MAR-1999
DEFINITION Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA,
            complete cds.
ACCESSION   AF022462
VERSION   AF022462.1 GI:2739005
KEYWORDS   .
SOURCE   Glycine max.
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 1824)
AUTHORS   Siminszky,B., Corbin,F.T., Ward,E.R., Fleischmann,T.J. and
            Dewey,R.E.
TITLE   Expression of a soybean cytochrome P450 monooxygenase cDNA in yeast
            and tobacco enhances the metabolism of phenylurea herbicides
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1750-1755 (1999)
MEDLINE   99145622
PUBMED   9990096
REFERENCE   2 (bases 1 to 1824)
AUTHORS   Siminszky,B., Dewey,R.E. and Corbin,F.T.
TITLE   Direct Submission
JOURNAL   Submitted (04-SEP-1997) Crop Science, North Carolina State
            University, Box 7620, Raleigh, NC 27695, USA
FEATURES   Location/Qualifiers
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     CDS   54..1619
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                     RVMAQGEAQKPLDLTEELLKWTNSTISMMLGEAEEIRDIAREVLKIFGEYSLTDFI
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Db    942  |||||||| ||  || ||||| ||||  |||| ||||| || || ||||||||||||| |||||
           CTTGTTGTCGACTTTTCTCGGCAGGAACAGACTCCACAGCGGTGCAACAGAGTGGGCA 1001

Qy   1098  CTGTCAGAGCTCATCAACAACACCCCAGGGTGTTGTTCAAAAGGCACAGAGAGATCGATGCC 1157
           || |||| ||||||||||| |||||  ||||| |||||  ||||||| || |||||| ||  |
Db   1002  TTGGCAGAACTCATCAACATCCTAAGTGTTGAAAAGGCTCGTGAGGAGGTCTACAGT 1061

Qy   1158  GTCGTGGGAAAAGACAGACTCGTTGACGAGGCAGATGTCCAGAACCTTCCTTACATTAGA 1217
           || ||||||||||||| |||||| ||  | ||||||||||||||||||||||||||||||
Db   1062  GTTGTGGGAAAGGACAGACGTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGA 1121

Qy   1218  TCCATCGTGAAGGAGGACGTTCCGCATGCACCCACCACTACCCGTGGTCAAAAGAAAGTGC 1277
           ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1122  GCAATCGTGAAGGAGACATTCCGCATGCACCCCAGTCCCAGTGGTCAAAAGAAAGTGC 1181

Qy   1278  GTGCAGGAGTGTGAGGTCGCACGGTTATGTGATCCCAGAGGGAGCATTGATCCTTTTCAAT 1337
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Db   1182  ACAGAAGAGTGTGAGATTAATGGATATGTGATCCCCAGAGGAGCATTGATCCTTCTTCAAT 1241

Qy   1338  GTTTGGGCCCTGGAAGAGACCCAAAATACTGGGACAGAGGCCACTGAGTTCCGTCCCGAA 1397
           || |||||||||||||||||||| |||||||||||||||||||| || ||||||||||||
Db   1242  GTATGCAAGTAGGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAG 1301

Qy   1398  AGGTTCTTAGAAAATGTGGGTGAAGGGATCAAG---CCGTTGACCTTAGGGGTCAACAT 1454
           |||| |||||  ||||||| ||||||||||| ||  ||||||| |||||| |||||||||
Db   1302  AGGTTCCTAGAGACAGAGCAGGGGCTGAAGGGAGCAGGCCCTCTTGATCTTAGGGGACAAACAT 1361

Qy   1455  TTCCAACTTCTTCCGTTCGGTCTCGGAAGGAGGATGTGCCCCTGGCGTCAATTTGGCCACT 1514
           || |||||  || ||||||||| ||||||||||| |||  |||||| ||||| |||||||||
Db   1362  TTTCAACTTCTCCCCATTTGGGTCTGGGAGAATGTGCCCCTGGAGTGCCCCAAGTTGGCTGGGT 1421

Qy   1515  GCGGGAATGGCCACACTGCTTGCGTCAGTTGCTTTGATCTCAGCGTAGTGGGC 1574
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Db   1422  TCGGGAATGGCAACACTTCTTGCATCTCTTATTCAGTTGCTTCGAAGTGCTGGGT 1481

Qy   1575  CCACAGGGAAAGATATTGAAGGGCCAATGATGCCAAGGTTAGCATGGGAAGGAGAGAGCCTGGA 1634
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Db   1482  CCACAAGGACAGATATTGAAGGGTGTGACGACAAAGTTAGCATGGGAAGGAGAGCCCGGC 1541

Qy   1635  CTCACGGTTCCAAGGGCACATAACCTCATCTGTGTCCCCGGTTGCGAAGATCAAGTGCCGTA 1694
           ||||| ||||||| ||||||||| ||  ||||||  |  ||| ||| | |||  |  ||
Db   1542  CTCACTGTTCCAAGGGCACTAGTCTGCTTGCTGTGTTCCACTTGCAAGGATCGGCGTTGCA 1601

Qy   1695  CCCAAACTCTTTCGTCGTAAA 1716
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Db   1602  TCTAAACTCCTTTCTTTAATTAA 1623
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RESULT 9
AF195799.
DEFINITION   AF195799    Glycine max isoflavone synthase 2 (ifs2) mRNA, complete cds.
ACCESSION    AF195799
VERSION      AF195799.1  GI:6979521
KEYWORDS     .
SOURCE       Glycine max.
ORGANISM     Glycine max
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
             Glycine.
REFERENCE    1  (bases 1 to 1824)
AUTHORS      Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
             McGonigle,B.
TITLE        Identification and expression of isoflavone synthase, the key
             enzyme for biosynthesis of isoflavones in legumes
JOURNAL      Nat. Biotechnol. 18 (2), 208-212 (2000)
MEDLINE      20124255
PUBMED       10657130
REFERENCE    2  (bases 1 to 1824)
AUTHORS      Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
TITLE        Direct Submission
JOURNAL      Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
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                     /gene="ifs2"
     CDS             54..1619
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                     IGHLHLLKDKLLHYALIDLSKKHGPLFSLYFGSMPTVVASTPELFKLFLQTHEATSFN
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                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMLGEAEEIRDIAREVLKIFGEYSLTDEI
                     WPLKHLKVGKYKRIDDILNKFDPVERVIKKRREIVRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPLPVVKRKCTEECEINGVVIPEGAL
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BASE COUNT   497 a     448 c     416 g     463 t
ORIGIN
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Query Match        54.7%;      Score 1036.8;     DB 8;     Length 1824;
Best Local Similarity  79.4%;   Pred. No. 1.4e-287;
Matches 1256;   Conservative   0;   Mismatches 317;   Indels   9;   Gaps   2;

Qy   138  AACACCATGTTGGTGGAACTTGCAATTACTCTGTTGGTGATAGCCCTGTTCATCACACCTG 197
          |||||| |||| | |||| | ||||||||| || | ||||||||||||||||||||||||
Db    48  AACACGATGTTGCTGAACTTGCACTTGGTTTATTGGTTTGGCTCTGTTCTGCACTTG 107

Qy   198  CGTCCCACTCAAGTGCAAAATCAAAGTCCCTTCGCACCTCCAAACCTTCCAAGTCCA 257
          |||||| |||| ||||||||| |  |||||||||||| |||||||| |||| |||||||
Db   108  CGTCCCACACCCTGCAAAATCAAAAGCACTTCGCCATCTCCAAACCACCAAGCCCA 167

Qy   258  AAACCCGTCACCATTGTGGGTCACTTTAGACAAACCCCTTCCCACTAC 317
          || ||| ||  || ||||||||||| || ||  |  ||||||||||||
Db   168  AAGCCTCGTCTCCTTCCCTTCCATAGGACACCTTAAAAGACAAACTTCCCACTAC 227

Qy   318  TCCCTCATCGACCTAAGCAAACGTATAGTGCCGTTACTCCCTCACTTCGGTTCCATG 377
          ||||  | |||| ||| ||||||||| |||  ||  |||||| |||| |||||||||
Db   228  GCACTCATCGACCTCTCCAAAAAAACATGGTCCCTTATTCTCTCTCTTACTTGGCTCCATG 287

Qy   378  CCAACCTGTGTAGCCTCCACCCCTCGAACTTTCAAACTTTCCTCCCAAACTCACGAGGCC 437
          ||||||  |  ||||| | ||||||||| | ||| ||| | |||| |||| |||||||||
Db   288  CCAACCGTTGTTGCCTCCAACAAGTTCAAGCTGTTCAAGCTCTTCCTCCAAACGCACGAGGCA 347

Qy   438  TCTTCCTTCAACACAAGTTCAAACCTCTGCCATTAGGCGCCTAACCTACGACAACTCT 497
          ||||||||||||| || ||||||| | ||| || |||| |||| ||  || |  ||
Db   348  ACTTCCTTCAACACAAGTTCCAAACCTCCAGCCATAAGCGCCTCACCTATGATAGCTCA 407

Qy   498  GTTGCCATGGTTCCCTTTGGTCCTTACTGGAAGTTCATTAGGAAGCTCATCATGAACGAC 557
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Db   408  GTGGCCATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGATC 467

Qy   558  CTCCTAAATGCCACAACTGTGACAAGTTGAGGCCTTTAAGGAGCCAAGAAATCCGAAAG 617
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Db   468  CTTCCAAGGCCCACCACTGTAAACAAGTTGAGGACCCAACAGACCCGCCAAG 527

Qy   618  GTCCTCAGGGTGATGGCACAGAGTGCTGAGTCCCAGCTCCAGGTCCACGAGGAG 677
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Db   528  TTCCTTAGGGTTATGGCCCAGGGCACCAGAAGCCCCCTTGACTTGACCGAGGAG 587

Qy   678  CTTCTCAAGTGGACCAACAGCACCATCTCGAGATGATGCTTGGGGAAGCAGAGGAAATC 737
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Db   588  CTTCTGAAATGGACCAACAAGCACCATCTCCATGATGATGCTCGGCGAGGCGAGGAGATC 647

Qy   738  AGGGACATAGCACGTGAGGTCTTAAGATCTTTGGGGAGTATAGTCTCACCGACTTCATC 797
          || |||| ||  || |||| || |||||||||||||| ||||| ||||||| ||||||||
Db   648  AGAGACATCGCTCGCGAGGTTCTTAAGATCTTTGGAATACAGCAGCCTGACTTCATC 707
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